SCORE Search Results Details for Application 10606302 and Search Result us-10-606-302a-10.rst.

<u>Score Home Page</u> <u>Retrieve Application List</u> <u>SCORE System Overview</u> <u>SCORE FAQ</u> <u>Comments / Suggestions</u>

This page gives you Search Results detail for the Application 10606302 and Search Result us-10-606-302a-10.rst.
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                   GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:          August 15, 2006, 10:05:07 ; Search time 9053.07 Seconds
                                             (without alignments)
                                             13094.897 Million cell updates/sec

Title:           US-10-606-302A-10
Perfect score:   2120
Sequence:        1 ggatcctcctgatcactgga..........accaagatgttccagctacc 2120

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters:     96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       EST:*
                 1:   gb_est1:*
                 2:   gb_est3:*
                 3:   gb_est4:*
                 4:   gb_est5:*
                 5:   gb_est6:*
                 6:   gb_htc:*
                 7:   gb_est2:*
                 8:   gb_est7:*
                 9:   gb_est8:*
                 10:  gb_est9:*
                 11:  gb_gss1:*
                 12:  gb_gss2:*
                 13:  gb_gss3:*
                 14:  gb_gss4:*

        Pred. No. is the number of results predicted by chance to have a
```

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1565.6	73.8	2247	6	AK167460	AK167460 Mus muscu
2	1564	73.8	2269	6	AK077740	AK077740 Mus muscu
3	754.2	35.6	760	8	CO565622	CO565622 AGENCOURT
4	699.2	33.0	790	8	CO572777	CO572777 AGENCOURT
5	690.8	32.6	782	8	CO574051	CO574051 AGENCOURT
6	679.8	32.1	794	8	CO567769	CO567769 AGENCOURT
7	664.4	31.3	1317	10	DV789420	DV789420 Hw_liver_
8	634.8	29.9	808	8	CO573278	CO573278 AGENCOURT
9	632	29.8	886	5	CF551083	CF551083 AGENCOURT
10	631.2	29.8	738	8	CO574740	CO574740 AGENCOURT
11	625.2	29.5	793	2	BI217680	BI217680 602934527
12	597.8	28.2	840	10	DV813743	DV813743 LB01711.C
13	596.4	28.1	744	8	CV114224	CV114224 AGENCOURT
14	592.4	27.9	594	8	CO556968	CO556968 AGENCOURT
15	580.2	27.4	792	8	CO425730	CO425730 UI-M-HU0-
16	579.6	27.3	867	2	BI218342	BI218342 602937723
17	578.8	27.3	758	9	DN119973	DN119973 1119949 M
18	573.6	27.1	872	4	CA752105	CA752105 UI-M-FD0-
19	573.4	27.0	735	10	DT889191	DT889191 1466050 M
20	569.8	26.9	797	1	AI097875	AI097875 ue40h10.y
21	563	26.6	670	2	BI331204	BI331204 602985159
22	549.8	25.9	831	8	CO567345	CO567345 AGENCOURT
23	549.2	25.9	618	8	CN724649	CN724649 E0883A09-
24	546.4	25.8	821	3	BP442620	BP442620 BP442620
25	538.4	25.4	886	3	BQ946437	BQ946437 AGENCOURT
c 26	536.2	25.3	840	9	DN120322	DN120322 1120333 M
27	528.4	24.9	719	2	BI146400	BI146400 602910767
28	526.4	24.8	951	7	BF533689	BF533689 602074093
c 29	522	24.6	682	4	CB421561	CB421561 594587 MA
30	521.4	24.6	728	2	BI145731	BI145731 602909885
31	519.6	24.5	770	2	BI149152	BI149152 602914216
32	514	24.2	826	2	BI731492	BI731492 603354382
33	498.2	23.5	949	4	BX849476	BX849476 BX849476
34	497.4	23.5	962	7	BF233498	BF233498 602024290
c 35	495	23.3	578	8	CO560193	CO560193 AGENCOURT
36	492	23.2	645	9	DN129329	DN129329 1143472 M
37	491.2	23.2	746	8	CO570899	CO570899 AGENCOURT
38	487.6	23.0	740	2	BI145941	BI145941 602911272
39	486.6	23.0	763	4	CB949170	CB949170 AGENCOURT
40	484.2	22.8	778	2	BI146017	BI146017 602911373
41	481.4	22.7	749	10	DV812815	DV812815 LB0147.CR
42	481.2	22.7	1036	7	BF533289	BF533289 602073744
43	475.4	22.4	956	2	BI328145	BI328145 602985402
44	474.6	22.4	665	3	BQ109198	BQ109198 imageqc_6
45	470.6	22.2	726	10	DT723071	DT723071 LB0142.CR

ALIGNMENTS

RESULT 1
AK167460
LOCUS   AK167460   2247 bp   mRNA   linear   HTC 21-SEP-2005

SCORE Search Results Details for Application 10606302 and Search Result us-10-606-302a-10.rnpbn.

This page gives you Search Results detail for the Application 10606302 and Search Result us-10-6(302a-10.rnpbn.

start

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OM nucleic - nucleic search, using sw model

Run on:         August 15, 2006, 14:38:19 ; Search time 393.828 Seconds
                                            (without alignments)
                                            8548.706 Million cell updates/sec

Title:          US-10-606-302A-10
Perfect score:  2120
Sequence:       1 ggatcctcctgatcactgga..........accaagatgttccagctacc 2120

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       2200221 seqs, 794037843 residues

Total number of hits satisfying chosen parameters:      4400442

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Published_Applications_NA_New:*
                1:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                2:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                3:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                4:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                5:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                6:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                7:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                8:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
                9:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
                10:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                            SUMMARIES
```

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                     %
  Result          Query
     No.   Score  Match Length DB  ID                    Description
        ------------------------------------------------------------------------
       1  470.4   22.2    668  6   US-10-488-619-2085    Sequence 2085, Ap
       2  466.8   22.0    510  6   US-10-488-619-2087    Sequence 2087, Ap
  c    3  365.4   17.2    791  6   US-10-488-619-2086    Sequence 2086, Ap
  c    4    346   16.3    733  6   US-10-488-619-2084    Sequence 2084, Ap
       5   90.8    4.3   2152  6   US-10-449-902-27255   Sequence 27255, A
       6   84.4    4.0   2420  9   US-11-218-305-19629   Sequence 19629, A
       7   77.4    3.7   1581  8   US-11-217-529-1906    Sequence 1906, Ap
       8   73.8    3.5   1581  8   US-11-217-529-77873   Sequence 77873, A
       9   45.4    2.1   1561  6   US-10-449-902-6166    Sequence 6166, Ap
      10   45.4    2.1   1740  6   US-10-449-902-6130    Sequence 6130, Ap
  c   11   44.6    2.1   2741  9   US-11-218-305-22630   Sequence 22630, A
  c   12   42.6    2.0   1234  6   US-10-449-902-6007    Sequence 6007, Ap
      13   42.6    2.0   2059  6   US-10-449-902-8518    Sequence 8518, Ap
      14   42.2    2.0   2120  8   US-11-266-748A-70478  Sequence 70478, A
      15   42.2    2.0   2120  8   US-11-266-748A-106039 Sequence 106039,
  c   16   42.2    2.0   2120  8   US-11-266-748A-123289 Sequence 123289,
      17   41.8    2.0   1176  8   US-11-217-529-81002   Sequence 81002, A
  c   18   41.2    1.9   2133  9   US-11-348-413-1505    Sequence 1505, Ap
      19     41    1.9   1334  6   US-10-449-902-21405   Sequence 21405, A
      20   39.8    1.9    657  8   US-11-266-748A-163252 Sequence 163252,
  c   21   39.6    1.9    787  8   US-11-266-748A-175933 Sequence 175933,
      22   39.6    1.9   1672  6   US-10-449-902-15918   Sequence 15918, A
      23   39.2    1.8   1658  9   US-11-174-307B-3883   Sequence 3883, Ap
      24     39    1.8   2087  6   US-10-449-902-9658    Sequence 9658, Ap
      25   38.8    1.8    741  6   US-10-374-780A-1007   Sequence 1007, Ap
      26   38.8    1.8   4453  9   US-11-218-305-17561   Sequence 17561, A
      27   38.4    1.8    936  8   US-11-266-748A-60691  Sequence 60691, A
      28   38.4    1.8   1000  8   US-11-266-748A-290001 Sequence 290001,
  c   29   38.4    1.8   1000  8   US-11-266-748A-341430 Sequence 341430,
      30   38.4    1.8   1307  8   US-11-266-748A-258261 Sequence 258261,
  c   31   38.4    1.8   1307  8   US-11-266-748A-318778 Sequence 318778,
  c   32   38.4    1.8   2412  8   US-11-266-748A-258884 Sequence 258884,
      33   38.4    1.8   2412  8   US-11-266-748A-319401 Sequence 319401,
      34   38.4    1.8   2427  9   US-11-384-733-2       Sequence 2, Appli
  c   35   38.4    1.8   5338  8   US-11-266-748A-29879  Sequence 29879, A
  c   36   38.2    1.8   2154  9   US-11-218-305-23430   Sequence 23430, A
      37     38    1.8   1529  9   US-11-218-305-14820   Sequence 14820, A
      38   37.8    1.8   1381  9   US-11-056-355B-12335  Sequence 12335, A
      39   37.8    1.8   1452  9   US-11-218-305-1646    Sequence 1646, Ap
      40   37.6    1.8    913  8   US-11-266-748A-161902 Sequence 161902,
      41   37.6    1.8   8404  8   US-11-266-748A-28705  Sequence 28705, A
      42   37.6    1.8   8833  6   US-10-505-928-785     Sequence 785, App
      43   37.6    1.8   8833  8   US-11-266-748A-29245  Sequence 29245, A
      44   37.6    1.8   8833  8   US-11-266-748A-31810  Sequence 31810, A
      45   37.6    1.8   8833  8   US-11-266-748A-56209  Sequence 56209, A
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ALIGNMENTS

RESULT 1
US-10-488-619-2085
; Sequence 2085, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;   APPLICANT: Greenlee, Winner and Sullivan, P.C.
;   TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Association

SCORE Search Results Details for Application 10€ and Search Result us-10-606-302a-10.rnpbı

This page gives you Search Results detail for the Application 10606302 and Search Result us-10-6(10.rnpbm.

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OM nucleic - nucleic search, using sw model

Run on:         August 15, 2006, 13:10:24 ; Search time 2658.71 Seconds
                                            (without alignments)
                                            9797.893 Million cell updates/sec

Title:          US-10-606-302A-10
Perfect score:  2120
Sequence:       1 ggatcctcctgatcactgga..........accaagatgttccagctacc 2120

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:      37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Published_Applications_NA_Main:*
                1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                10:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                11:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                12:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                13:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                14:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
                15:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
                16:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
```

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
	1	2120	100.0	2120	9	US-10-606-300-10	Sequence 10, Appl
	2	2120	100.0	2120	10	US-10-606-302-10	Sequence 10, Appl
	3	1323	62.4	1323	3	US-09-917-800A-1694	Sequence 1694, Ap
	4	592	27.9	688	8	US-10-404-460-106	Sequence 106, App
c	5	324	15.3	384	3	US-09-917-800A-659	Sequence 659, App
	6	203.6	9.6	242	3	US-09-960-352-12740	Sequence 12740, A
c	7	169	8.0	201	3	US-09-864-408A-2307	Sequence 2307, Ap
	8	164.6	7.8	1317	7	US-10-156-761-2396	Sequence 2396, Ap
	9	164.6	7.8	9025608	7	US-10-156-761-1	Sequence 1, Appli
	10	120.4	5.7	1284	3	US-09-894-844-106	Sequence 106, App
	11	120.4	5.7	1284	8	US-10-388-902-106	Sequence 106, App
	12	120.4	5.7	1284	8	US-10-647-089-106	Sequence 106, App
	13	120.4	5.7	1284	16	US-11-143-401-106	Sequence 106, App
	14	118	5.6	248	8	US-10-430-201-3718	Sequence 3718, Ap
	15	118	5.6	248	8	US-10-430-201-3719	Sequence 3719, Ap
	16	111	5.2	128	7	US-10-388-934-131	Sequence 131, App
	17	111	5.2	128	16	US-11-224-663-131	Sequence 131, App
	18	111	5.2	128	16	US-11-224-525-131	Sequence 131, App
c	19	98	4.6	1000	10	US-10-750-185-41341	Sequence 41341, A
c	20	98	4.6	1000	10	US-10-750-623-41341	Sequence 41341, A
	21	94.4	4.5	2034	6	US-10-234-026-12	Sequence 12, Appl
	22	94.4	4.5	2064	9	US-10-606-300-4	Sequence 4, Appli
	23	94.4	4.5	2064	10	US-10-606-302-4	Sequence 4, Appli
	24	92.4	4.4	2142	8	US-10-437-963-16021	Sequence 16021, A
	25	84.4	4.0	3069	9	US-10-425-115-63810	Sequence 63810, A
	26	78.2	3.7	1833	9	US-10-606-300-2	Sequence 2, Appli
	27	78.2	3.7	1833	10	US-10-606-302-2	Sequence 2, Appli
	28	77.4	3.7	1581	11	US-10-932-182A-1906	Sequence 1906, Ap
	29	73.8	3.5	1581	9	US-10-606-300-6	Sequence 6, Appli
	30	73.8	3.5	1581	10	US-10-606-302-6	Sequence 6, Appli
	31	73.8	3.5	1581	11	US-10-932-182A-77873	Sequence 77873, A
	32	73.8	3.5	2138	9	US-10-606-300-8	Sequence 8, Appli
	33	73.8	3.5	2138	10	US-10-606-302-8	Sequence 8, Appli
	34	73	3.4	1066	8	US-10-424-599-24226	Sequence 24226, A
	35	64.4	3.0	409	12	US-10-301-480-273360	Sequence 273360,
	36	64.4	3.0	409	12	US-10-301-480-886769	Sequence 886769,
	37	64.4	3.0	420	4	US-09-925-065A-182834	Sequence 182834,
	38	64.4	3.0	420	5	US-09-925-065A-182834	Sequence 182834,
	39	61.8	2.9	321	3	US-09-770-517C-7	Sequence 7, Appli
	40	61.8	2.9	321	8	US-10-750-026-7	Sequence 7, Appli
	41	55.4	2.6	696	8	US-10-767-701-2324	Sequence 2324, Ap
	42	54.2	2.6	1266	7	US-10-156-761-2078	Sequence 2078, Ap
c	43	52.2	2.5	545	6	US-10-027-632-5229	Sequence 5229, Ap
c	44	52.2	2.5	545	7	US-10-027-632-5229	Sequence 5229, Ap
	45	51.4	2.4	532	6	US-10-027-632-57456	Sequence 57456, A

ALIGNMENTS

RESULT 1
US-10-606-300-10
; Sequence 10, Application US/10606300
; Publication No. US20050019879A1

SCORE Search Results Details for Application 10606302 and Search Result us-10-606-302a-10.rni.

This page gives you Search Results detail for the Application 10606302 and Search Result us-10-6(302a-10.rni.

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OM nucleic - nucleic search, using sw model

Run on:          August 15, 2006, 11:29:45 ; Search time 277.821 Seconds
                                              (without alignments)
                                              14278.103 Million cell updates/sec

Title:           US-10-606-302A-10
Perfect score:   2120
Sequence:        1 ggatcctcctgatcactgga..........accaagatgttccagctacc 2120

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters:      2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_NA:*
                 1:  /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
                 2:  /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
                 3:  /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                 4:  /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                 5:  /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                 6:  /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                 7:  /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                 8:  /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                 9:  /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                 10:  /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                         SUMMARIES
```

```
                         %
     Result          Query
        No.   Score  Match Length DB   ID                      Description
     ------------------------------------------------------------------------------
          1   2120   100.0   2120  3   US-09-630-983A-10       Sequence 10, Appl
          2   120.4    5.7   1284  3   US-09-894-844-106       Sequence 106, App
          3   120.4    5.7   1932  3   US-09-252-991A-7271     Sequence 7271, Ap
          4   120.4    5.7 4403765  3   US-09-103-840A-2        Sequence 2, Appli
          5   120.4    5.7 4411529  3   US-09-103-840A-1        Sequence 1, Appli
   c      6   101.8    4.8   1392  3   US-09-252-991A-7430     Sequence 7430, Ap
          7    94.4    4.5   2034  3   US-09-423-468A-12       Sequence 12, Appl
          8    94.4    4.5   2064  3   US-09-630-983A-4        Sequence 4, Appli
          9    78.2    3.7   1833  3   US-09-630-983A-2        Sequence 2, Appli
         10    73.8    3.5   1581  3   US-09-630-983A-6        Sequence 6, Appli
         11    73.8    3.5   2138  3   US-09-630-983A-8        Sequence 8, Appli
         12    61.8    2.9    321  3   US-09-770-517C-7        Sequence 7, Appli
         13    61.8    2.9    321  3   US-10-750-026-7         Sequence 7, Appli
         14    60.2    2.8   7218  2   US-08-232-463-14        Sequence 14, Appl
         15    51.4    2.4   1185  3   US-09-248-796A-3166     Sequence 3166, Ap
         16    45      2.1   1089  3   US-09-252-991A-1313     Sequence 1313, Ap
         17    45      2.1   3981  3   US-09-252-991A-1361     Sequence 1361, Ap
   c     18    45      2.1   4179  3   US-09-252-991A-1244     Sequence 1244, Ap
         19    43.8    2.1   2037  3   US-09-902-540-6164      Sequence 6164, Ap
   c     20    43.8    2.1   2039  3   US-09-902-540-304       Sequence 304, App
         21    43.2    2.0   3120  3   US-09-423-468A-14       Sequence 14, Appl
         22    42.2    2.0   3776  3   US-09-900-237-3         Sequence 3, Appli
         23    41.4    2.0   4187  4   US-09-880-107-1609      Sequence 1609, Ap
         24    41      1.9   1419  3   US-09-266-965-61        Sequence 61, Appl
         25    41      1.9   1499  3   US-09-902-540-6928      Sequence 6928, Ap
         26    41      1.9   3465  3   US-09-902-540-596       Sequence 596, App
   c     27    41      1.9  53500  3   US-09-266-965-76        Sequence 76, Appl
         28    40.6    1.9   1566  3   US-09-252-991A-1548     Sequence 1548, Ap
   c     29    40.6    1.9   1611  3   US-09-252-991A-1569     Sequence 1569, Ap
         30    40.6    1.9   2088  3   US-09-252-991A-1453     Sequence 1453, Ap
         31    40.6    1.9   3568  3   US-10-160-719A-1        Sequence 1, Appli
         32    40.6    1.9   3568  3   US-10-209-059-41        Sequence 41, Appl
         33    39.6    1.9   1314  3   US-09-252-991A-16243    Sequence 16243, A
         34    39.6    1.9   1500  3   US-09-252-991A-16352    Sequence 16352, A
   c     35    39.6    1.9   1584  3   US-09-252-991A-16239    Sequence 16239, A
         36    39      1.8   1602  3   US-09-124-541-10        Sequence 10, Appl
         37    39      1.8   1602  3   US-09-663-326-10        Sequence 10, Appl
   c     38    38.8    1.8    505  3   US-09-621-976-15639     Sequence 15639, A
         39    38.4    1.8   1026  3   US-09-902-540-3767      Sequence 3767, Ap
         40    38.4    1.8   1185  3   US-09-023-339-3         Sequence 3, Appli
         41    38.4    1.8   1185  4   US-10-077-381-14        Sequence 14, Appl
         42    38.4    1.8   1260  3   US-09-023-173-5         Sequence 5, Appli
         43    38.4    1.8   1308  3   US-09-023-173-10        Sequence 10, Appl
         44    38.4    1.8   1308  3   US-09-023-339-6         Sequence 6, Appli
         45    38.4    1.8   1664  3   US-09-438-917-5         Sequence 5, Appli
```

ALIGNMENTS

RESULT 1
US-09-630-983A-10
; Sequence 10, Application US/09630983A
; Patent No. 6630330
; GENERAL INFORMATION:
; APPLICANT: Porro, Danilo
; APPLICANT: Sauer, Michael

SCORE Search Results Details for Application 10606302 and Search Result us-10-606-302a-10.rng.

Score Home Page   Retrieve Application List   SCORE System Overview   SCORE FAQ   Comments / Suggestions

This page gives you Search Results detail for the Application 10606302 and Search Result us-10-606-302a-10.rng.

start

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OM nucleic - nucleic search, using sw model

Run on:          August 15, 2006, 09:24:26 ; Search time 1194.93 Seconds
                                             (without alignments)
                                             12369.931 Million cell updates/sec

Title:           US-10-606-302A-10
Perfect score:   2120
Sequence:        1 ggatcctcctgatcactgga..........accaagatgttccagctacc 2120

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:      10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       N_Geneseq_8:*
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                 2:   geneseqn1990s:*
                 3:   geneseqn2000s:*
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                 12:  geneseqn2004as:*
                 13:  geneseqn2004bs:*
                 14:  geneseqn2005s:*
                 15:  geneseqn2006s:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2120	100.0	2120	1	AAN92440	Aan92440 DNA seque
2	2120	100.0	2120	6	ABK10124	Abk10124 Rat cDNA
3	1323	62.4	1323	6	ABK63787	Abk63787 Rat seque
4	1323	62.4	1323	10	ADB58424	Adb58424 Toxicity-
5	1323	62.4	1323	10	ADB53007	Adb53007 Primary r
6	1323	62.4	1323	13	ADT71411	Adt71411 Rat L-gul
7	1319.8	62.3	1323	2	AAT87005	Aat87005 DNA encod
8	592	27.9	688	6	ABT09006	Abt09006 Phase-1 R
9	592	27.9	688	10	ADG30926	Adg30926 Liver tox
10	592	27.9	688	12	ADG45513	Adg45513 Liver inf
11	592	27.9	688	13	ADR91163	Adr91163 Spleen ne
12	470.4	22.2	668	10	ADD34307	Add34307 Mouse mit
13	466.8	22.0	510	10	ADD34309	Add34309 Mouse mit
c 14	365.4	17.2	791	10	ADD34308	Add34308 Mouse mit
c 15	346	16.3	733	10	ADD34306	Add34306 Mouse mit
c 16	324	15.3	384	6	ABK62752	Abk62752 Rat seque
c 17	324	15.3	384	10	ADB56666	Adb56666 Toxicity-
18	203.6	9.6	242	8	ABX47575	Abx47575 Bovine ES
c 19	169	8.0	201	6	ABN76207	Abn76207 Human ORF
20	156.8	7.4	167	6	ABN16596	Abn16596 Human ORF
21	120.4	5.7	1284	13	ADR96680	Adr96680 M. tuberc
22	120.4	5.7	1932	11	ABD08667	Abd08667 Pseudomon
23	120.4	5.7	110000	4	AAI99682_19	Continuation (20 o
24	120.4	5.7	110000	4	AAI99682_20	Continuation (21 o
25	120.4	5.7	110000	4	AAI99683_19	Continuation (20 o
26	120.4	5.7	110000	4	AAI99683_20	Continuation (21 o
27	118	5.6	248	12	ADL87326	Adl87326 DNA up-re
28	118	5.6	248	12	ADL87325	Adl87325 DNA up-re
29	113.4	5.3	713	6	ABL60142	Abl60142 Fungi str
30	111	5.2	128	11	ADW21752	Adw21752 Rat hepat
c 31	101.8	4.8	1392	11	ABD08826	Abd08826 Pseudomon
32	94.4	4.5	2034	2	AAV69438	Aav69438 Cauliflow
33	94.4	4.5	2064	6	ABK10121	Abk10121 B. olerac
34	90.8	4.3	2023	2	AAX31915	Aax31915 L-galacto
35	78.2	3.7	1833	6	ABK10120	Abk10120 A. thalia
36	73.8	3.5	1581	6	ABK10122	Abk10122 Yeast cDN
37	73.8	3.5	1591	4	AAF58029	Aaf58029 S cerevis
38	73.8	3.5	2138	6	ABK10123	Abk10123 Yeast cDN
39	65	3.1	1248	2	AAV11297	Aav11297 Nucleotid
40	63.4	3.0	720	2	AAV11295	Aav11295 N-termina
41	62.6	3.0	1386	4	AAF76931	Aaf76931 Penicilli
42	62.6	3.0	1443	4	AAF76930	Aaf76930 Penicilli
43	62.6	3.0	1774	4	AAF76929	Aaf76929 Penicilli
44	61.8	2.9	321	4	AAH43266	Aah43266 D-aminoac
c 45	58.4	2.8	2000	8	ADA71938	Ada71938 Rice gene

ALIGNMENTS

RESULT 1
AAN92440

SCORE Search Results Details for Application 10606302 and Search Result us-10-606-302a-10.rge.

This page gives you Search Results detail for the Application 10606302 and Search Result us-10-606-302a-10.rge.

start

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OM nucleic - nucleic search, using sw model

Run on:         August 15, 2006, 09:51:39 ; Search time 12121 Seconds
                                           (without alignments)
                                           11184.560 Million cell updates/sec

Title:          US-10-606-302A-10
Perfect score:  2120
Sequence:       1 ggatcctcctgatcactgga..........accaagatgttccagctacc 2120

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:      12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      GenEmbl:*
                1:  gb_env:*
                2:  gb_pat:*
                3:  gb_ph:*
                4:  gb_pl:*
                5:  gb_pr:*
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                11:  gb_ov:*
                12:  gb_htg:*
                13:  gb_in:*
                14:  gb_om:*
                15:  gb_ba:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2120	100.0	2120	2	CS017724	CS017724 Sequence
2	2120	100.0	2120	2	E01923	E01923 cDNA encodi
3	2120	100.0	2120	2	AR405969	AR405969 Sequence
4	2120	100.0	2120	2	AX374957	AX374957 Sequence
5	2120	100.0	2120	6	RATFLAVIN	J03536 Rat L-gulon
6	2087.6	98.5	2192	6	BC089803	BC089803 Rattus no
7	1565.6	73.8	2240	6	BC028828	BC028828 Mus muscu
8	1564	73.8	2227	6	BC019856	BC019856 Mus muscu
9	1564	73.8	2235	6	BC028822	BC028822 Mus muscu
10	1475.4	69.6	2035	6	BC034835	BC034835 Mus muscu
11	1323	62.4	1323	2	AX402018	AX402018 Sequence
12	1319.8	62.3	1323	2	A93824	A93824 Sequence 3
13	1188.6	56.1	1323	6	AY453064	AY453064 Mus muscu
14	1058.6	49.9	1939	14	AF440259	AF440259 Sus scrof
15	1031.2	48.6	2127	14	BC102936	BC102936 Bos tauru
16	879.8	41.5	6009	6	D12754	D12754 Rattus norv
c 17	879.8	41.5	239102	12	AC137051	AC137051 Rattus no
18	879.8	41.5	267809	12	AC137461	AC137461 Rattus no
19	714.2	33.7	1976	11	BC084892	BC084892 Xenopus 1
20	642.2	30.3	1747	11	AY039838	AY039838 Scyliorhi
21	592	27.9	688	2	AX525572	AX525572 Sequence
c 22	480.2	22.7	141017	6	AC126444	AC126444 Mus muscu
c 23	480.2	22.7	191606	6	AC126272	AC126272 Mus muscu
24	473.8	22.3	605	14	AF185292	AF185292 Bos tauru
25	441	20.8	847	11	BX933840	BX933840 Gallus ga
26	329	15.5	727	11	BX934260	BX934260 Gallus ga
c 27	324	15.3	384	2	AX400983	AX400983 Sequence
28	321.2	15.2	661	6	BC035221	BC035221 Mus muscu
29	290.6	13.7	2095	13	AK115232	AK115232 Ciona int
30	177.2	8.4	110000	15	CP000088_22	Continuation (23 o
c 31	169	8.0	201	2	AX309322	AX309322 Sequence
32	164.6	7.8	110000	15	BA000030_29	Continuation (30 o
c 33	162	7.6	295150	15	SCO939125	AL939125 Streptomy
34	156.8	7.4	167	2	CQ435909	CQ435909 Sequence
c 35	150.2	7.1	110000	15	CP000249_03	Continuation (4 of
c 36	150.2	7.1	110000	15	CP000249_04	Continuation (5 of
c 37	142.4	6.7	190294	12	AC158696	AC158696 Bos tauru
38	142.4	6.7	270496	12	AC163911	AC163911 Bos tauru
39	134.8	6.4	190294	12	AC158696	AC158696 Bos tauru
40	134.4	6.3	4612	6	D12762	D12762 Cavia porce
41	134	6.3	158	14	AF136938	AF136938 Sus scrof
c 42	133.6	6.3	110000	4	AE016819_12	Continuation (13 o
43	121.8	5.7	110000	15	AP006618_46	Continuation (47 o
44	120.4	5.7	1284	2	AR456097	AR456097 Sequence
45	120.4	5.7	110000	15	AE000516_19	Continuation (20 o

ALIGNMENTS

RESULT 1
CS017724

SCORE Search Results Details for Application 10606302 and Search Result us-10-606-302a-8.rst.

This page gives you Search Results detail for the Application 10606302 and Search Result us-10-606-302a-8.rst.

start

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OM nucleic - nucleic search, using sw model

Run on:          August 15, 2006, 10:05:07 ; Search time 9129.93 Seconds
                                            (without alignments)
                                            13094.897 Million cell updates/sec

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Scoring table:   IDENTITY_NUC
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Searched:        48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters:      96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       EST:*
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                 2:   gb_est3:*
                 3:   gb_est4:*
                 4:   gb_est5:*
                 5:   gb_est6:*
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                 7:   gb_est2:*
                 8:   gb_est7:*
                 9:   gb_est8:*
                 10:  gb_est9:*
                 11:  gb_gss1:*
                 12:  gb_gss2:*
                 13:  gb_gss3:*
                 14:  gb_gss4:*

       Pred. No. is the number of results predicted by chance to have a
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	457.6	21.4	961	14	CNS06DEH	AL393711 T7 end of
c	2	323.2	15.1	1098	14	CNS06LXM	AL404768 T3 end of
	3	304.8	14.3	1084	14	CNS076UF	AL431869 T7 end of
c	4	282.6	13.2	553	11	BZ305138	BZ305138 KD3345.q1
	5	133.2	6.2	869	10	DR640257	DR640257 EST103088
	6	126.8	5.9	972	10	DR634104	DR634104 EST102472
c	7	121.8	5.7	940	14	CNS06H1S	AL398438 T3 end of
	8	108.8	5.1	1005	14	CNS07050	AL423202 T7 end of
	9	93.4	4.4	581	11	BZ301673	BZ301673 KD1411.p1
	10	82.4	3.9	927	1	AL667095	AL667095 AL667095
	11	75.6	3.5	728	2	BI145731	BI145731 602909885
	12	75.4	3.5	2247	6	AK167460	AK167460 Mus muscu
	13	75.4	3.5	2269	6	AK077740	AK077740 Mus muscu
	14	75.2	3.5	886	5	CF551083	CF551083 AGENCOURT
	15	74.8	3.5	671	3	BW342883	BW342883 BW342883
	16	74	3.5	792	8	CO425730	CO425730 UI-M-HU0-
	17	74	3.5	808	8	CO573278	CO573278 AGENCOURT
	18	74	3.5	872	4	CA752105	CA752105 UI-M-FD0-
	19	74	3.5	886	3	BQ946437	BQ946437 AGENCOURT
	20	73.6	3.4	808	4	CB558176	CB558176 AGENCOURT
c	21	73.4	3.4	588	3	BU698006	BU698006 LL2in1000
	22	73.4	3.4	815	3	BU904729	BU904729 AGENCOURT
	23	73.2	3.4	840	4	CB559648	CB559648 AGENCOURT
c	24	72.4	3.4	514	3	BU698976	BU698976 LL2in1424
	25	72.4	3.4	935	8	CV437826	CV437826 EST891739
c	26	72	3.4	570	3	BU695653	BU695653 LL2in1199
	27	71.6	3.3	886	8	CN240306	CN240306 EST006166
c	28	71.4	3.3	537	3	BU697932	BU697932 LL2in1415
	29	71.2	3.3	878	4	CB559873	CB559873 AGENCOURT
	30	71.2	3.3	907	5	CD791363	CD791363 EST662724
	31	70.8	3.3	734	5	CF521421	CF521421 AGENCOURT
	32	70.8	3.3	797	1	AI097875	AI097875 ue40h10.y
c	33	70	3.3	674	3	BU699086	BU699086 LL2in1283
	34	70	3.3	754	5	CF519846	CF519846 AGENCOURT
	35	69.6	3.3	753	5	CF521358	CF521358 AGENCOURT
	36	69.6	3.3	907	3	BU904429	BU904429 AGENCOURT
	37	68.6	3.2	716	1	AI573803	AI573803 uj65h10.y
c	38	68.6	3.2	1101	14	CNS00EVL	AL069706 Drosophil
	39	68.2	3.2	641	7	AV976012	AV976012 AV976012
	40	67.8	3.2	760	8	CO565622	CO565622 AGENCOURT
	41	66.6	3.1	821	4	CA788084	CA788084 AGENCOURT
	42	66.4	3.1	719	2	BI146400	BI146400 602910767
	43	66.4	3.1	831	8	CO567345	CO567345 AGENCOURT
	44	66.4	3.1	867	2	BI218342	BI218342 602937723
	45	66.4	3.1	1036	7	BF533289	BF533289 602073744

ALIGNMENTS

RESULT 1
CNS06DEH
LOCUS   CNS06DEH   961 bp   DNA   linear   GSS 17-JUN-2001

SCORE Search Results Details for Application 10606302 and Search Result us-10-606-302a-8.rnpbn.

This page gives you Search Results detail for the Application 10606302 and Search Result us-10-6(302a-8.rnpbn.

start

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                    GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:         August 15, 2006, 14:38:19 ; Search time 397.172 Seconds
                                             (without alignments)
                                             8548.706 Million cell updates/sec

Title:          US-10-606-302A-8
Perfect score:  2138
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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       2200221 seqs, 794037843 residues

Total number of hits satisfying chosen parameters:      4400442

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Published_Applications_NA_New:*
                1:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                2:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                3:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                4:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                5:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                6:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                7:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                8:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
                9:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
                10:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES
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                     %
Result             Query
     No.   Score  Match Length DB   ID                          Description
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       1  1571.4   73.5   1581  8   US-11-217-529-77873         Sequence 77873, A
       2  1200.2   56.1   1581  8   US-11-217-529-1906          Sequence 1906, Ap
       3    132     6.2    939  8   US-11-217-529-77872         Sequence 77872, A
       4   80.8     3.8    939  8   US-11-217-529-1905          Sequence 1905, Ap
       5   60.2     2.8    668  6   US-10-488-619-2085          Sequence 2085, Ap
       6   49.4     2.3   7432  6   US-10-517-441-524           Sequence 524, App
       7   48.8     2.3   2987  6   US-10-517-441-345           Sequence 345, App
       8   48.6     2.3  16842  6   US-10-517-441-575           Sequence 575, App
  c    9    48      2.2  34088  8   US-11-266-748A-23848        Sequence 23848, A
      10   47.4     2.2  15355  6   US-10-517-441-689           Sequence 689, App
      11   47.4     2.2 106234  8   US-11-266-748A-24973        Sequence 24973, A
      12   47.2     2.2   2987  6   US-10-517-441-619           Sequence 619, App
      13    47      2.2  17897  6   US-10-517-441-618           Sequence 618, App
      14    46      2.2   2501  6   US-10-517-441-562           Sequence 562, App
      15    46      2.2   2501  6   US-10-517-441-609           Sequence 609, App
  c   16   45.8     2.1   4928  9   US-11-218-305-3816          Sequence 3816, Ap
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; Sequence 77873, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;   APPLICANT: SUNTORY LIMITED
;   APPLICANT: NAKAO, YOSHIHIRO

SCORE Search Results Details for Application 10606302 and Search Result us-10-606-302a 8.rnpbm.

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                        GenCore version 5.1.9
                Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:          August 15, 2006, 13:10:24 ; Search time 2681.29 Seconds
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	9	80.8	3.8	939	11	US-10-932-182A-1905	Sequence 1905, Ap
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SCORE Search Results Details for Application 10606302 and Search Result us-10-606-302a-8.

This page gives you Search Results detail for the Application 10606302 and Search Result us-10-6(8.rni.

start

Go Back to pre·

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OM nucleic - nucleic search, using sw model

Run on:         August 15, 2006, 11:29:45 ; Search time 280.179 Seconds
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; Sequence 8, Application US/09630983A
; Patent No. 6630330
; GENERAL INFORMATION:
;   APPLICANT: Porro, Danilo
;   APPLICANT: Sauer, Michael
;   TITLE OF INVENTION: Ascorbic Acid Production from Yeast
;   FILE REFERENCE: 2028.594000
;   CURRENT APPLICATION NUMBER: US/09/630,983A

SCORE Search Results Details for Application 10606302 and Search Result us-10-606-302a-8.rng.

This page gives you Search Results detail for the Application 10606302 and Search Result us-10-606-302a-8.rng.

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                        GenCore version 5.1.9
            Copyright (c) 1993 - 2006  Biocceleration Ltd.


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5	128.8	6.0	939	13	ADS47104	Ads47104 Bacterial
6	75.4	3.5	1323	2	AAT87005	Aat87005 DNA encod
7	73.8	3.5	1323	6	ABK63787	Abk63787 Rat seque
8	73.8	3.5	1323	10	ADB58424	Adb58424 Toxicity-
9	73.8	3.5	1323	10	ADB53007	Adb53007 Primary r
10	73.8	3.5	1323	13	ADT71411	Adt71411 Rat L-gul
11	73.8	3.5	2120	1	AAN92440	Aan92440 DNA seque
12	73.8	3.5	2120	6	ABK10124	Abk10124 Rat cDNA
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ALIGNMENTS

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SCORE Search Results Details for Application 106

This page gives you Search Results detail for the Application 10606302 and Search Result us-10-6(start

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                        GenCore version 5.1.9
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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       GenEmbl:*
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                 12:  gb_htg:*
                 13:  gb_in:*
                 14:  gb_om:*
                 15:  gb_ba:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                              SUMMARIES
                 %
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Result          Query
   No.    Score  Match Length DB  ID                    Description
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     1    2138   100.0   2138  2   CS017722              CS017722 Sequence
     2    2138   100.0   2138  2   AR405968              AR405968 Sequence
     3    2138   100.0   2138  2   AX374955              AX374955 Sequence
     4    2138   100.0   2138  4   AB009401              AB009401 Saccharom
c    5    2074.4  97.0  32148  4   SC9725                Z46660 S.cerevisia
     6    1967.6  92.0   2622  4   SCU40390              U40390 Saccharomyc
     7    1576.6  73.7   1591  2   AX077305              AX077305 Sequence
     8    1576.2  73.7   1581  2   CS017720              CS017720 Sequence
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    12     768.4  35.9 110000  4   CR382123_14           Continuation (15 o
c   13     756.6  35.4 110000  4   CR380954_03           Continuation (4 of
c   14     619.8  29.0 110000  4   AE016819_12           Continuation (13 o
    15     402.6  18.8   3762  4   AF031228              AF031228 Candida a
    16     334.2  15.6   1185  2   AR548035              AR548035 Sequence
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    19     190.6   8.9    713  2   AX461040              AX461040 Sequence
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    21     119.6   5.6 110000  4   AP007151_32           Continuation (33 o
    22     107.2   5.0 110000 15   BA000028_17           Continuation (18 o
c   23     105.4   4.9  36484  4   SPAPB1A10             AL512562 S.pombe c
    24      84     3.9   2095 13   AK115232              AK115232 Ciona int
    25      80.4   3.8   1747 11   AY039838              AY039838 Scyliorhi
c   26      78     3.6 105521 12   AC121064              AC121064 Magnaport
    27      77     3.6   2192  6   BC089803              BC089803 Rattus no
    28      75.4   3.5   1323  2   A93824                A93824 Sequence 3
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    30      75.4   3.5   2235  6   BC028822              BC028822 Mus muscu
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    32      73.8   3.5   1323  2   AX402018              AX402018 Sequence
    33      73.8   3.5   2120  2   CS017724              CS017724 Sequence
    34      73.8   3.5   2120  2   E01923                E01923 cDNA encodi
    35      73.8   3.5   2120  2   AR405969              AR405969 Sequence
    36      73.8   3.5   2120  2   AX374957              AX374957 Sequence
    37      73.8   3.5   2120  6   RATFLAVIN             J03536 Rat L-gulon
    38      73.8   3.5   2227  6   BC019856              BC019856 Mus muscu
    39      71.6   3.3   1976 11   BC084892              BC084892 Xenopus l
    40      69.6   3.3   2023  4   AB024527              AB024527 Nicotiana
    41      68.8   3.2 110000 15   AE016877_06           Continuation (7 of
    42      68.6   3.2   1951  4   AB048530              AB048530 Nicotiana
    43      67.8   3.2   2127 14   BC102936              BC102936 Bos tauru
c   44      64.4   3.0 110000 12   PFMAL8P1_06           Continuation (7 of
c   45      63.4   3.0 206154 11   BX465837              BX465837 Zebrafish
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ALIGNMENTS

RESULT 1
CS017722
LOCUS   CS017722   2138 bp   DNA   linear   PAT 15-FEB-2005
DEFINITION Sequence 8 from Patent EP1498489.
ACCESSION   CS017722
VERSION   CS017722.1 GI:59891083
KEYWORDS   .
SOURCE   Saccharomyces cerevisiae (baker's yeast)